Claims

1. A substantially pure human Bcl-X_L-binding polypeptide, said polypeptide consisting of the sequence of any of SEQ ID NOS: 4-50, 63-71, and 224-228.

2. A substantially pure human Bcl-X_L-binding polypeptide, said polypeptide comprising the sequence of any of SEQ ID NOS: 51-62, 229, and 230.

3. An isolated nucleic acid molecule encoding a polypeptide of claim 1 or 2.

4. The isolated nucleic acid of claim 3, wherein said nucleic acid molecule consists of the sequence of any of SEQ ID NOS: 156-202, 215-223, and 231-235.

5. The isolated nucleic acid of claim 3, wherein said nucleic acid molecule comprises the sequence of any of SEQ ID NOS: 203-214, 236, and 237.

6. A vector comprising the isolated nucleic acid molecule of claim 3.

7. A cell comprising the isolated nucleic acid molecule of claim 3.

8. A cell comprising the vector of claim 6.

9. A method of identifying a Bcl-X_L-binding polypeptide, said method comprising the steps of:

(a) providing a population of source labeled nucleic acid-protein fusion molecules;

(b) contacting said population of nucleic acid-protein fusion molecules with a Bcl-X_L polypeptide under conditions that allow interaction between the protein portion of a nucleic acid-protein fusion molecule of said population and said Bcl-X_L polypeptide;

(c) detecting an interaction between said protein portion and said Bcl-X_L polypeptide, thereby identifying a Bcl-X_L-binding polypeptide,

10. The method of claim 9, wherein said population of source labeled nucleic acid-protein fusion molecules is derived from more than one source.

11. The method of claim 9, wherein, in step (a), said nucleic acid-protein fusion molecules are detectably-labeled.

12. The method of claim 11, wherein, in step (b), said Bcl-X_L polypeptide is immobilized on a solid support; and wherein, in step (c), the detection of an interaction between said protein portion of a nucleic acid-protein fusion molecule and said Bcl-X_L polypeptide is carried out by detecting the labeled nucleic acid-protein fusion molecule bound to said solid support.

13. The method of claim 12, wherein said solid support is a chip or a bead.

14. A method of identifying a compound that modulates binding between a Bcl-X_L polypeptide and a Bcl-X_L-binding polypeptide, said method comprising the steps of:

(a) contacting a Bcl-X_L polypeptide with (i) a Bcl-X_L-binding polypeptide, said Bcl-X_L-binding polypeptide consisting of the sequence of any of SEQ ID NOS: 4-50, 63-71, and 224-228, and (ii) a candidate compound, under conditions that allow binding between said Bcl-X_L polypeptide and said Bcl-X_L-binding polypeptide;

(b) determining the level of binding between said Bcl-X_L polypeptide and said Bcl-X_L-binding polypeptide, wherein an increase or decrease in the level of binding between said Bcl-X_L polypeptide and said Bcl-X_L-binding polypeptide, relative to the level of binding between said Bcl-X_L polypeptide and said Bcl-X_L-binding polypeptide in the absence of said candidate compound, indicates a compound that modulates the binding between a Bcl-X_L polypeptide and a Bcl-X_L-binding polypeptide.

15. A method of identifying a compound that modulates binding between a Bcl-X_L polypeptide and a Bcl-X_L-binding polypeptide, said method comprising the steps of:

(a) contacting a Bcl-X_L polypeptide with (i) a Bcl-X_L-binding polypeptide, said Bcl-X_L-binding polypeptide comprising the sequence of any of SEQ ID NOS: 51-62, 229, and 230, and (ii) a candidate compound, under conditions that allow binding between said Bcl-X_L polypeptide and said Bcl-X_L-binding polypeptide;

(b) determining the level of binding between said Bcl-X_L polypeptide and said Bcl-X_L-binding polypeptide, wherein an increase or decrease in the level

of binding between said Bcl-X_L polypeptide and said Bcl-X_L-binding polypeptide, relative to the level of binding between said Bcl-X_L polypeptide and said Bcl-X_L-binding polypeptide in the absence of said candidate compound, indicates a compound that modulates the binding between a Bcl-X_L polypeptide and a Bcl-X_L-binding polypeptide.

16. The method of claim 14 or 15, wherein said Bcl-X_L-binding polypeptide is part of a nucleic acid-protein fusion molecule.

17. The method of claim 14 or 15, wherein, in step (a), said Bcl-X_L polypeptide is attached to a solid support.

18. The method of claim 17, wherein said Bcl-X_L-binding polypeptide is detectably-labeled; and, in step (b), said level of binding between said Bcl-X_L polypeptide and said Bcl-X_L-binding polypeptide is determined by measuring the amount of Bcl-X_L-binding protein that binds to said solid support.

19. The method of claim 17, wherein said solid support is a chip or a bead.

20. A method of source-labeling a nucleic acid-protein fusion molecule, said method comprising the steps of:

(a) providing an RNA molecule;

(b) generating a first cDNA strand from said RNA molecule;

(c) generating a second cDNA strand complementary to said first cDNA strand, wherein said second cDNA strand comprises a nucleic acid

sequence that identifies the source of said RNA molecule;

(d) generating an RNA molecule from the double stranded cDNA molecule of step (c)

(e) attaching a peptide acceptor to said RNA molecule of step (d);

(f) *in vitro* translating said RNA to generate a source labeled nucleic acid-protein fusion molecule.

21. A source-labeled nucleic acid-protein fusion molecule, said nucleic acid portion of said fusion molecule comprising a coding sequence for said protein and a label that identifies the source of said nucleic acid portion.

22. A method of identifying the source of the nucleic acid portion of a nucleic acid-protein fusion molecule, said method comprising the steps of:

(a) providing a population of nucleic acid-protein fusion molecules, said molecules comprising a source label that identifies the source of the nucleic acid portion of said nucleic acid-protein fusion molecules; and

(b) determining the identity of said source label, thereby identifying the source of the nucleic acid portion of a nucleic acid protein fusion molecule.

23. The method of claim 22, wherein said source label is cell type-specific.

24. The method of claim 22, wherein said source label is tissue-specific.

25. The method of claim 22, wherein said source label is species-

specific.

26. The method of claim 22, wherein said population of nucleic acid-protein fusion molecules contains subpopulations of nucleic acid-protein fusion molecules from a plurality of sources.